

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
- (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
INTERFERON
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Foley & Lardner
(B) STREET: 3000 K Street, N.W., Suite 500
(C) CITY: Washington
(D) STATE: D.C.
(E) ZIP: 20007
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/307,588
(B) FILING DATE: 05-DEC-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP93/00770
(B) FILING DATE: 30-MAR-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 92400902.0
(B) FILING DATE: 31-MAR-1992
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SAXE, Bernhard D.
(B) REGISTRATION NUMBER: 28,665
(C) REFERENCE/DOCKET NUMBER: 17283/117/GUPL
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202)672-5300
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1334

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C1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGCAGGGAT CTGCGGCGGC TCCAG	ATG ATG GTC GTC CTC CTG GGC GCG ACG	53
Met Met Val Val Leu Leu Gly Ala Thr	1 5	
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA	101	
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala	15 20 25	
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA	149	
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile	30 35 40	
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG	197	
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly	45 50 55	
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG	245	
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp	60 65 70	
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT	293	
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe	75 80 85	
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA	341	
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg	90 95 100 105	
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA	389	
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr	110 115 120	
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT	437	
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala	125 130 135	
GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT	485	
Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser	140 145 150	
GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC	533	
Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile	155 160 165	
TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC	581	
Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser	170 175 180 185	
AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA	629	
Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys	190 195 200	
GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA	677	
Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro	205 210 215	
GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA	725	
Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu	220 225 230	
AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT	773	
Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp	235 240 245	

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TAT	ACA	TAT	GCA	AAC	ATG	ACC	TTT	CAA	GTT	CAG	TGG	CTC	CAC	GCC	TTT	821
Tyr	Thr	Tyr	Ala	Asn	Met	Thr	Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	
250					255					260					265	
TTA	AAA	AGG	AAT	CCT	GGA	AAC	CAT	TTG	TAT	AAA	TGG	AAA	CAA	ATA	CCT	869
Leu	Lys	Arg	Asn	Pro	Gly	Asn	His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	
				270					275						280	
GAC	TGT	GAA	AAT	GTC	AAA	ACT	ACC	CAG	TGT	GTC	TTT	CCT	CAA	AAC	GTT	917
Asp	Cys	Glu	Asn	Val	Lys	Thr	Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	
			285					290					295			
TTC	CAA	AAA	GGA	ATT	TAC	CTT	CTC	CGC	GTA	CAA	GCA	TCT	GAT	GGA	AAT	965
Phe	Gln	Lys	Gly	Ile	Tyr	Leu	Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	
		300					305					310				
AAC	ACA	TCT	TTT	TGG	TCT	GAA	GAG	ATA	AAG	TTT	GAT	ACT	GAA	ATA	CAA	1013
Asn	Thr	Ser	Phe	Trp	Ser	Glu	Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	
	315					320					325					
GCT	TTC	CTA	CTT	CCT	CCA	GTC	TTT	AAC	ATT	AGA	TCC	CTT	AGT	GAT	TCA	1061
Ala	Phe	Leu	Leu	Pro	Pro	Val	Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	Ser	
	330				335					340					345	
TTC	CAT	ATC	TAT	ATC	GGT	GCT	CCA	AAA	CAG	TCT	GGA	AAC	ACG	CCT	GTG	1109
Phe	His	Ile	Tyr	Ile	Gly	Ala	Pro	Lys	Gln	Ser	Gly	Asn	Thr	Pro	Val	
				350					355					360		
ATC	CAG	GAT	TAT	CCA	CTG	ATT	TAT	GAA	ATT	ATT	TTT	TGG	GAA	AAC	ACT	1157
Ile	Gln	Asp	Tyr	Pro	Leu	Ile	Tyr	Glu	Ile	Ile	Phe	Trp	Glu	Asn	Thr	
			365					370					375			
TCA	AAT	GCT	GAG	AGA	AAA	ATT	ATC	GAG	AAA	AAA	ACT	GAT	GTT	ACA	GTT	1205
Ser	Asn	Ala	Glu	Arg	Lys	Ile	Ile	Glu	Lys	Lys	Thr	Asp	Val	Thr	Val	
		380					385					390				
CCT	AAT	TTG	AAA	CCA	CTG	ACT	GTA	TAT	TGT	GTG	AAA	GCC	AGA	GCA	CAC	1253
Pro	Asn	Leu	Lys	Pro	Leu	Thr	Val	Tyr	Cys	Val	Lys	Ala	Arg	Ala	His	
		395				400					405					
ACC	ATG	GAT	GAA	AAG	CTG	AAT	AAA	AGC	AGT	GTT	TTT	AGT	GAC	GCT	GTA	1301
Thr	Met	Asp	Glu	Lys	Leu	Asn	Lys	Ser	Ser	Val	Phe	Ser	Asp	Ala	Val	
					415					420					425	
TGT	GAG	AAA	ACA	AAA	CCA	GGA	AAT	ACC	TCT	AAA	TGAGGTACC					1343
Cys	Glu	Lys	Thr	Lys	Pro	Gly	Asn	Thr	Ser	Lys						
				430					435							

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Met	Val	Val	Leu	Leu	Gly	Ala	Thr	Thr	Leu	Val	Leu	Val	Ala	Val
1				5					10					15	
Gly	Pro	Trp	Val	Leu	Ser	Ala	Ala	Ala	Gly	Gly	Lys	Asn	Leu	Lys	Ser
			20					25					30		

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
210 215 220

Val Glu Asn Glu Leu Pro Pro Glu Asn Ile Glu Val Ser Val Gln
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile
370 375 380

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Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr
385 390 395 400
Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn
405 410 415
Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430
Asn Thr Ser Lys
435

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1755 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTGCAGGGAT CTGCGGCGGC TCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG	53
Met Met Val Val Leu Leu Gly Ala Thr	
1 5	
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA	101
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala	
10 15 20 25	
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA	149
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile	
30 35 40	
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG	197
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly	
45 50 55	
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG	245
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp	
60 65 70	
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT	293
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe	
75 80 85	
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA	341
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg	
90 95 100 105	
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA	389
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr	
110 115 120	
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT	437
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala	
125 130 135	

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GAA	GAT	AAG	GCA	ATA	GTG	ATA	CAC	ATC	TCT	CCT	GGA	ACA	AAA	GAT	AGT	485
Glu	Asp	Lys	Ala	Ile	Val	Ile	His	Ile	Ser	Pro	Gly	Thr	Lys	Asp	Ser	
		140					145					150				
GTT	ATG	TGG	GCT	TTG	GAT	GGT	TTA	AGC	TTT	ACA	TAT	AGC	TTA	CTT	ATC	533
Val	Met	Trp	Ala	Leu	Asp	Gly	Leu	Ser	Phe	Thr	Tyr	Ser	Leu	Leu	Ile	
	155					160					165					
TGG	AAA	AAC	TCT	TCA	GGT	GTA	GAA	GAA	AGG	ATT	GAA	AAT	ATT	TAT	TCC	581
Trp	Lys	Asn	Ser	Ser	Gly	Val	Glu	Glu	Arg	Ile	Glu	Asn	Ile	Tyr	Ser	
	170				175					180					185	
AGA	CAT	AAA	ATT	TAT	AAA	CTC	TCA	CCA	GAG	ACT	ACT	TAT	TGT	CTA	AAA	629
Arg	His	Lys	Ile	Tyr	Lys	Leu	Ser	Pro	Glu	Thr	Thr	Tyr	Cys	Leu	Lys	
			190						195				200			
GTT	AAA	GCA	GCA	CTA	CTT	ACG	TCA	TGG	AAA	ATT	GGT	GTC	TAT	AGT	CCA	677
Val	Lys	Ala	Ala	Leu	Leu	Thr	Ser	Trp	Lys	Ile	Gly	Val	Tyr	Ser	Pro	
		205					210					215				
GTA	CAT	TGT	ATA	AAG	ACC	ACA	GTT	GAA	AAT	GAA	CTA	CCT	CCA	CCA	GAA	725
Val	His	Cys	Ile	Lys	Thr	Thr	Val	Glu	Asn	Glu	Leu	Pro	Pro	Pro	Glu	
		220					225					230				
AAT	ATA	GAA	GTC	AGT	GTC	CAA	AAT	CAG	AAC	TAT	GTT	CTT	AAA	TGG	GAT	773
Asn	Ile	Glu	Val	Ser	Val	Gln	Asn	Gln	Asn	Tyr	Val	Leu	Lys	Trp	Asp	
	235					240					245					
TAT	ACA	TAT	GCA	AAC	ATG	ACC	TTT	CAA	GTT	CAG	TGG	CTC	CAC	GCC	TTT	821
Tyr	Thr	Tyr	Ala	Asn	Met	Thr	Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	
	250				255					260					265	
TTA	AAA	AGG	AAT	CCT	GGA	AAC	CAT	TTG	TAT	AAA	TGG	AAA	CAA	ATA	CCT	869
Leu	Lys	Arg	Asn	Pro	Gly	Asn	His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	
				270				275						280		
GAC	TGT	GAA	AAT	GTC	AAA	ACT	ACC	CAG	TGT	GTC	TTT	CCT	CAA	AAC	GTT	917
Asp	Cys	Glu	Asn	Val	Lys	Thr	Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	
			285					290					295			
TTC	CAA	AAA	GGA	ATT	TAC	CTT	CTC	CGC	GTA	CAA	GCA	TCT	GAT	GGA	AAT	965
Phe	Gln	Lys	Gly	Ile	Tyr	Leu	Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	
		300					305					310				
AAC	ACA	TCT	TTT	TGG	TCT	GAA	GAG	ATA	AAG	TTT	GAT	ACT	GAA	ATA	CAA	1013
Asn	Thr	Ser	Phe	Trp	Ser	Glu	Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	
	315					320					325					
GCT	TTC	CTA	CTT	CCT	CCA	GTC	TTT	AAC	ATT	AGA	TCC	CTT	AGT	GAT	TCA	1061
Ala	Phe	Leu	Leu	Pro	Pro	Val	Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	Ser	
	330				335					340					345	
TTC	CAT	ATC	TAT	ATC	GGT	GCT	CCA	AAA	CAG	TCT	GGA	AAC	ACG	CCT	GTG	1109
Phe	His	Ile	Tyr	Ile	Gly	Ala	Pro	Lys	Gln	Ser	Gly	Asn	Thr	Pro	Val	
				350					355					360		
ATC	CAG	GAT	TAT	CCA	CTG	ATT	TAT	GAA	ATT	ATT	TTT	TGG	GAA	AAC	ACT	1157
Ile	Gln	Asp	Tyr	Pro	Leu	Ile	Tyr	Glu	Ile	Ile	Phe	Trp	Glu	Asn	Thr	
			365					370					375			
TCA	AAT	GCT	GAG	AGA	AAA	ATT	ATC	GAG	AAA	AAA	ACT	GAT	GTT	ACA	GTT	1205
Ser	Asn	Ala	Glu	Arg	Lys	Ile	Ile	Glu	Lys	Lys	Thr	Asp	Val	Thr	Val	
		380					385					390				
CCT	AAT	TTG	AAA	CCA	CTG	ACT	GTA	TAT	TGT	GTG	AAA	GCC	AGA	GCA	CAC	1253
Pro	Asn	Leu	Lys	Pro	Leu	Thr	Val	Tyr	Cys	Val	Ala	Ala	Arg	Ala	His	
		395				400					405					

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ACC ATG GAT GAA AAG GTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA 1301
 Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val
 410 415 420 425

TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA ATT TGG CTT ATA GTT 1349
 Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val
 430 435 440

GGA ATT TGT ATT GCA TTA TTT GCT CTC CCG TTT GTC ATT TAT GCT GCG 1397
 Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala
 445 450 455

AAA GTC TTC TTG AGA TGC ATC AAT TAT GTC TTC TTT CCA TCA CTT AAA 1445
 Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys
 460 465 470

CCT TCT TCC AGT ATA GAT GAG TAT TTC TCT GAA CAG CCA TTG AAG AAT 1493
 Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn
 475 480 485

CTT CTG CTT TCA ACT TCT GAG GAA CAA ATC GAA AAA TGT TTC ATA ATT 1541
 Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile
 490 495 500 505

GAA AAT ATA AGC ACA ATT GCT ACA GTA GAA GAA ACT AAT CAA ACT GAT 1589
 Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp
 510 515 520

GAA GAT CAT AAA AAA TAC AGT TCC CAA ACT AGC CAA GAT TCA GGA AAT 1637
 Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn
 525 530 535

TAT TCT AAT GAA GAT GAA AGC GAA AGT AAA ACA AGT GAA GAA CTA CAG 1685
 Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln
 540 545 550

CAG GAC TTT GTA TGACCAGAAA TGAAGTGTGT CAAGTATAAG GTTTTTTCAGC 1737
 Gln Asp Phe Val
 555

AGGAGTTACA CTGGTACC 1755

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val
 1 5 10 15

Gly Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser
 20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
 35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
 50 55 60

Tyr	Gln	Lys	Thr	Gly	Met	Asp	Asn	Trp	Ile	Lys	Leu	Ser	Gly	Cys	Gln	
65					70					75					80	
Asn	Ile	Thr	Ser	Thr	Lys	Cys	Asn	Phe	Ser	Ser	Leu	Lys	Leu	Asn	Val	
				85					90					95		
Tyr	Glu	Glu	Ile	Lys	Leu	Arg	Ile	Arg	Ala	Glu	Lys	Glu	Asn	Thr	Ser	
			100					105					110			
Ser	Trp	Tyr	Glu	Val	Asp	Ser	Phe	Thr	Pro	Phe	Arg	Lys	Ala	Gln	Ile	
		115					120					125				
Gly	Pro	Pro	Glu	Val	His	Leu	Glu	Ala	Glu	Asp	Lys	Ala	Ile	Val	Ile	
	130					135					140					
His	Ile	Ser	Pro	Gly	Thr	Lys	Asp	Ser	Val	Met	Trp	Ala	Leu	Asp	Gly	
145					150					155					160	
Leu	Ser	Phe	Thr	Tyr	Ser	Leu	Leu	Ile	Trp	Lys	Asn	Ser	Ser	Gly	Val	
				165					170					175		
Glu	Glu	Arg	Ile	Glu	Asn	Ile	Tyr	Ser	Arg	His	Lys	Ile	Tyr	Lys	Leu	
			180					185					190			
Ser	Pro	Glu	Thr	Thr	Tyr	Cys	Leu	Lys	Val	Lys	Ala	Ala	Leu	Leu	Thr	
		195					200					205				
Ser	Trp	Lys	Ile	Gly	Val	Tyr	Ser	Pro	Val	His	Cys	Ile	Lys	Thr	Thr	
	210					215					220					
Val	Glu	Asn	Glu	Leu	Pro	Pro	Pro	Glu	Asn	Ile	Glu	Val	Ser	Val	Gln	
225					230					235					240	
Asn	Gln	Asn	Tyr	Val	Leu	Lys	Trp	Asp	Tyr	Thr	Tyr	Ala	Asn	Met	Thr	
				245					250					255		
Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	Leu	Lys	Arg	Asn	Pro	Gly	Asn	
			260					265					270			
His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	Asp	Cys	Glu	Asn	Val	Lys	Thr	
	275						280					285				
Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	Phe	Gln	Lys	Gly	Ile	Tyr	Leu	
	290					295					300					
Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	Asn	Thr	Ser	Phe	Trp	Ser	Glu	
305					310					315					320	
Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	Ala	Phe	Leu	Leu	Pro	Pro	Val	
				325					330					335		
Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	Ser	Phe	His	Ile	Tyr	Ile	Gly	Ala	
			340					345					350			
Pro	Lys	Gln	Ser	Gly	Asn	Thr	Pro	Val	Ile	Gln	Asp	Tyr	Pro	Leu	Ile	
		355					360					365				
Tyr	Glu	Ile	Ile	Phe	Trp	Glu	Asn	Thr	Ser	Asn	Ala	Glu	Arg	Lys	Ile	
	370					375					380					
Ile	Glu	Lys	Lys	Thr	Asp	Val	Thr	Val	Pro	Asn	Leu	Lys	Pro	Leu	Thr	
385					390					395				400		
Val	Tyr	Cys	Val	Lys	Ala	Arg	Ala	His	Thr	Met	Asp	Glu	Lys	Leu	Asn	
				405					410					415		

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Sub 1

Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430
Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile Cys Ile Ala Leu Phe
435 440 445
Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile
450 455 460
Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu
465 470 475 480
Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu
485 490 495
Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala
500 505 510
Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp His Lys Lys Tyr Ser
515 520 525
Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser
530 535 540
Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp Phe Val
545 550 555

Sub C1

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WRITEENABLE
WRITEPROTECT

~~BENOIT, et al.~~

FILED:05-DEC-1994

AGAINST THE INTERFERON..."

~~DATA REC'D: 26 MAR 1996~~